

#13



PCT09

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,388

DATE: 03/13/2002

TIME: 13:44:49

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\03132002\I869388.raw

5 <110> APPLICANT: Bates, Elizabeth
6 Fournier, Nathalie
7 Chalus, Lionel
8 Garrone, Pierre

10 <120> TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND METHODS

12 <130> FILE REFERENCE: SF0977X
14 <140> CURRENT APPLICATION NUMBER: 09/869,388
C--> 15 <141> CURRENT FILING DATE: 2002-02-21
17 <160> NUMBER OF SEQ ID NOS: 14
19 <170> SOFTWARE: IBM PC compatible
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1249
23 <212> TYPE: DNA
24 <213> ORGANISM: homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (154)..(1062)
30 <220> FEATURE:
31 <221> NAME/KEY: sig_peptide
32 <222> LOCATION: (154)..(210)
34 <220> FEATURE:
35 <221> NAME/KEY: mat_peptide
36 <222> LOCATION: (211)..(1062)
38 <400> SEQUENCE: 1

39	gtttggggaa ggctcctggc cccacagcc ctcttcggag cctgagcccg gctctcctca	60
41	ctcacctcaa cccccaggcg gccctccac agggcccctc tcttgccctgg acggctctgc	120
43	tggtctcccc gtcccctgga gaagaacaag gcc atg ggt cgg ccc ctg ctg ctg	174
44	Met Gly Arg Pro Leu Leu Leu	
45	-19 -15	
47	ccc cta ctg ccc ctg ctg ctg ccg cca gca ttt ctg cag cct agt ggc	222
48	Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly	
49	-10 -5 1	
51	tcc aca gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa	270
52	Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys	
53	5 10 15 20	
55	cac ctg tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc	318
56	His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe	
57	25 30 35	
59	tat tac ccc tgg gag tta gcc aca gct ccc gac gtg aga ata tcc tgg	366
60	Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp	
61	40 45 50	
63	aga cgg ggc cac ttc cac ggg cag tcc ttc tac agc aca agg ccg cct	414
64	Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro	

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65          55          60          65
67 tcc att cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag      462
68 Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu
69          70          75          80
71 ggt cag aag agc ggc ttc ctc agg atc tcc aac ctg cag aag cag gac      510
72 Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp
73 85          90          95          100
75 cag tct gtg tat ttc tgc cga gtt gag ctg gac aca cgg agc tca ggg      558
76 Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly
77          105          110          115
79 agg cag cag tgg cag tcc atc gag ggg acc aaa ctc tcc atc acc cag      606
80 Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln
81          120          125          130
83 gct gtc acg acc acc acc cag agg ccc agc agc atg act acc acc tgg      654
84 Ala Val Thr Thr Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp
85          135          140          145
87 agg ctc agt agc aca acc acc aca acc ggc ctc agg gtc aca cag ggc      702
88 Arg Leu Ser Ser Thr Thr Thr Thr Thr Gly Leu Arg Val Thr Gln Gly
89          150          155          160
91 aaa cga cgc tca gac tct tgg cac ata agt ctg gag act gct gtg ggg      750
92 Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly
93 165          170          175          180
95 gtg gca gtg gct gtc act gtg ctc gga atc atg att ttg gga ctg atc      798
96 Val Ala Val Ala Val Thr Val Leu Gly Ile Met Ile Leu Gly Leu Ile
97          185          190          195
99 tgc ctc ctc agg tgg agg aga agg aaa ggt cag cag cgg act aaa gcc      846
100 Cys Leu Leu Arg Trp Arg Arg Arg Lys Gly Gln Gln Arg Thr Lys Ala
101          200          205          210
103 aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag      894
104 Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu
105          215          220          225
107 aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag      942
108 Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys
109          230          235          240
112 gat gac ggc atc gta tat gct tcc ctt gcc ctc tcc agc tcc acc tca      990
113 Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser
114 245          250          255          260
116 ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac gag      1038
117 Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu
118          265          270          275
120 acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa      1092
121 Thr Leu Tyr Ser Val Leu Lys Ala
122          280
124 tgggtaggcc aggtacagtg gcgcacacct gtaatcccag ctactctgaa gcctgaggca      1152
126 gaatcaagtg agcccaggag ttcagggcca gctttgataa tggagcgaga tgccatctct      1212
128 agttaaaaaat atatattaac aataaagtaa caaatatt      1249
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 303
133 <212> TYPE: PRT

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Input Set : A:\seqlist.txt

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134 <213> ORGANISM: homo sapiens
136 <400> SEQUENCE: 2
137 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu Pro Pro
138 -19 -15 -10 -5
140 Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu
141 1 5 10
143 Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser
144 15 20 25
146 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala
147 30 35 40 45
149 Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser
150 50 55 60
152 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg
153 65 70 75
155 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile
156 80 85 90
158 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu
159 95 100 105
161 Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly
162 110 115 120 125
164 Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Thr Gln Arg Pro
165 130 135 140
167 Ser Ser Met Thr Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr
168 145 150 155
170 Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile
171 160 165 170
173 Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly
174 175 180 185
176 Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys
177 190 195 200 205
179 Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln
180 210 215 220
182 Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr
183 225 230 235
185 Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu
186 240 245 250
188 Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro
189 255 260 265
191 Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala
192 270 275 280
195 <210> SEQ ID NO: 3
196 <211> LENGTH: 943
197 <212> TYPE: DNA
198 <213> ORGANISM: homo sapiens
200 <220> FEATURE:
201 <221> NAME/KEY: CDS
202 <222> LOCATION: (130)..(819)
204 <220> FEATURE:
205 <221> NAME/KEY: sig_peptide

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 TIME: 13:44:49

Input Set : A:\seqlist.txt
 Output Set: N:\CRF3\03132002\I869388.raw

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206 <222> LOCATION: (130)..(180)
208 <220> FEATURE:
209 <221> NAME/KEY: mat_peptide
210 <222> LOCATION: (181)..(819)
212 <400> SEQUENCE: 3
213 acagccctct tggagcctc agcccggctc tctcactca cctcaacccc caggcggccc      60
215 ctccacaggg cccctctcct gctggacgg ctctgctggt ctccccgtcc cctggagaag      120
217 aacaaggcc atg ggt cgg ccc ctg ctg ctg ccc cta ctg ccc ctg ctg      168
218           Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu
219           -17      -15      -10      -5
221 ctg ccg cca gca ttt ctg cag cct agt ggc tcc aca gga tct ggt cca      216
222 Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro
223           1           5           10
225 agc tac ctt tat ggg gtc act caa cca aaa cac ctc tca gcc tcc atg      264
226 Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met
227           15           20           25
229 ggt ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta      312
230 Gly Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu
231           30           35           40
233 gcc aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac      360
234 Ala Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His
235 45           50           55           60
237 ggg cag tcc ttc tac agc aca agg ccg cct tcc att cac aag gat tat      408
238 Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr
239           65           70           75
241 gtg aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc      456
242 Val Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe
243           80           85           90
245 ctc agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc      504
246 Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys
247           95           100           105
249 cga gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc      552
250 Arg Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser
251           110           115           120
253 atc gag ggg acc aaa ctc tcc atc acc cag ggt cag cag cgg act aaa      600
254 Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys
255 125           130           135           140
257 gcc aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat      648
258 Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr
259           145           150           155
261 gag aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc      696
262 Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro
263           160           165           170
265 aag gat gac ggc atc gtc tat gct tcc ctt gcc ctc tcc agc tcc acc      744
266 Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr
267           175           180           185
269 tca ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac      792
270 Ser Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn
271           190           195           200

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VERIFICATION SUMMARY

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Input Set : A:\seqlist.txt

Output Set: N:\CRF3\03132002\I869388.raw

L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:772 M:112 C: (48) String data converted to lower case,
L:780 M:112 C: (48) String data converted to lower case,
L:788 M:112 C: (48) String data converted to lower case,
L:796 M:112 C: (48) String data converted to lower case,



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Team: OIPEBackFileIndexing
Dossier: 09869388

Legal Date: 02-21-2002

No.	Doccode	Number of pages
1	A...	2
2	ABST	1
3	REM	1
4	PA..	1
5	SEQLIST	14

Total number of pages: 19

Remarks:

Order of re-scan issued on